

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Martin Roland Jensen
Soren Mouritsen
Henrik Elsner
Iben Dalum



(ii) TITLE OF INVENTION: Modified human TNF-alpha molecules, DNA encoding them, and vaccines containing said modified TNF-alpha or DNA

(iii) NUMBER OF SEQUENCES: 42

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Farmaceutisk Laboratorium Ferring A/S
(B) STREET: Indertoften 10
(C) CITY: Vanloese
(E) COUNTRY: Denmark
(F) POSTAL CODE (ZIP): DK-2720

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/060,294
(B) FILING DATE: 15-APR-1998

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/044,187
(B) FILING DATE: 24-APR-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Price, D. Douglas
(B) REGISTRATION NUMBER: 24,514
(C) REFERENCE/DOCKET NUMBER: P60953US1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (202) 638-6666
(B) TELEFAX: (202) 393-5350

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..477

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION:/codon_start= 1

/function= "Antigen"

/product= "TNF-alpha analog"

/evidence= EXPERIMENTAL

/gene= "tnfp2-1"

/standard_name= "TNF2-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT CAG TAC ATT AAA GCC AAT 48
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Gln Tyr Ile Lys Ala Asn
1 5 10 15

TCT AAA TTC ATC GGT ATA ACT GAG CTG CAG CTC CAG TGG CTG AAC CGC 96
Ser Lys Phe Ile Gly Ile Thr Glu Leu Gln Leu Gln Trp Leu Asn Arg
20 25 30

CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG 144
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
35 40 45

CTG GTG GTG CCA TCA GAG GGC CTG TAC CTC ATC TAC TCC CAG GTC CTC 192
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
50 55 60

TTC AAG GGC CAA GGC TGC CCC TCC ACC CAT GTG CTC CTC ACC CAC ACC 240
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
65 70 75 80

ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT 288
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
85 90 95

GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC 336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
100 105 110

AAG CCC TGG TAT GAG CCC ATC TAT CTG GGA GGG GTC TTC CAG CTG GAG 384
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
115 120 125

AAG GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG CCC GAC TAT CTC GAC 432
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
130 135 140

TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC TAG 477
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *
145 150 155

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Val Arg Ser Ser Ser Arg Thr Pro Ser Gln Tyr Ile Lys Ala Asn
1 5 10 15
Ser Lys Phe Ile Gly Ile Thr Glu Leu Gln Leu Gln Trp Leu Asn Arg
20 25 30
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
35 40 45
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
50 55 60
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
65 70 75 80
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
85 90 95
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
100 105 110
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
115 120 125
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
130 135 140
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *
145 150 155

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..477
(D) OTHER INFORMATION: /codon_start= 1

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/function= "Antigen"
/product= "TNF-alpha analog"
/gene= "tnfP2-3"
/standard_name= "TNF2-3"

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT GAC AAG CCT GTA GCC CAT	48
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
160 165 170 175	
GTT GTA GCA AAC CCT CAA GCT GAG GGG CAG CTC CAG TGG CTG AAC CGC	96
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
180 185 190	
CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG	144
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
195 200 205	
CTG GTG GTG CCA TCA GAG GGC CTG TAC CTC ATC TAC TCC CAG GTC CTC	192
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
210 215 220	
TTC CAG TAC ATA AAG GCC AAC TCC AAG TTT ATC GGC ATC ACC GAG CTC	240
Phe Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu	
225 230 235	
ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT	288
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
240 245 250 255	
GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC	336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
260 265 270	
AAG CCC TGG TAT GAG CCC ATC TAT CTG GGA GGG GTC TTC CAG CTG GAG	384
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	
275 280 285	
AAG GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG CCC GAC TAT CTC GAC	432
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	
290 295 300	
TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC TAG	477
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *	
305 310 315	

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His

1	5	10	15
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	20	25	30
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	35	40	45
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	50	55	60
Phe Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu	65	70	75
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	85	90	95
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	100	105	110
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	115	120	125
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	130	135	140
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *	145	150	155

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..477
- (D) OTHER INFORMATION: /codon_start= 1
/function= "Antigen"
/product= "TNF-alpha analog"
/gene= "tnfp2-4"
/standard_name= "TNF2-4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT GAC AAG CCT GTA GCC CAT
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His

160	165	170	175	
GTT GTA GCA AAC CCT CAA GCT GAG GGG CAG CTC CAG TGG CTG AAC CGC				96
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	180	185	190	
CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG				144
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	195	200	205	
CTG GTG GTG CCA TCA GAG GGC CTG TAC CTC ATC TAC TCC CAG GTC CTC				192
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	210	215	220	
TTC AAG GGC CAA GGC TGC CCC TCC ACC CAT GTG CTC CTC ACC CAC ACC				240
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr	225	230	235	
ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT				288
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	240	245	250	255
GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC				336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	260	265	270	
AAG CCC CAG TAT ATC AAG GCC AAT TCG AAA TTC ATC GGC ATC ACG GAG				384
Lys Pro Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu	275	280	285	
CTC GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG CCC GAC TAT CTC GAC				432
Leu Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	290	295	300	
TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC TAG				477
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *	305	310	315	

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met	Val	Arg	Ser	Ser	Ser	Arg	Thr	Pro	Ser	Asp	Lys	Pro	Val	Ala	His
1				5					10					15	
Val	Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg
			20					25					30		
Arg	Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln
		35					40					45			
Leu	Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu
	50					55					60				

Phe	Lys	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr	
65					70					75					80	
Ile	Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu	Leu	Ser	
				85					90					95		
Ala	Ile	Lys	Ser	Pro	Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala	
			100					105					110			
Lys	Pro	Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr	Glu	
		115					120					125				
Leu	Gly	Asp	Arg	Leu	Ser	Ala	Glu	Ile	Asn	Arg	Pro	Asp	Tyr	Leu	Asp	
	130					135					140					
Phe	Ala	Glu	Ser	Gly	Gln	Val	Tyr	Phe	Gly	Ile	Ile	Ala	Leu	*		
145					150					155						

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..477
- (D) OTHER INFORMATION:/function= "Antigen"
/product= "TNF-alpha analog"
/gene= "tnfp2-5"
/standard_name= "TNF2-5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATG	GTC	AGA	TCA	TCT	TCT	CGA	ACC	CCG	AGT	GAC	AAG	CCT	GTA	GCC	CAT	48
Met	Val	Arg	Ser	Ser	Ser	Arg	Thr	Pro	Ser	Asp	Lys	Pro	Val	Ala	His	
160					165					170					175	
GTT	GTA	GCA	AAC	CCT	CAA	GCT	GAG	GGG	CAG	CTC	CAG	TGG	CTG	AAC	CGC	96
Val	Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg	
			180					185						190		
CGG	GCC	AAT	GCC	CTC	CTG	GCC	AAT	GGC	GTG	GAG	CTG	AGA	GAT	AAC	CAG	144
Arg	Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	
			195					200					205			
CTG	GTG	GTG	CCA	TCA	GAG	GGC	CTG	TAC	CTC	ATC	TAC	TCC	CAG	GTC	CTC	192
Leu	Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	

210	215	220	
TTC AAG GGC CAA GGC TGC CCC TCC ACC CAT GTG CTC CTC ACC CAC ACC			240
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr			
225	230	235	
ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT			288
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser			
240	245	250	255
GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC			336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala			
260	265	270	
AAG CCC TGG TAT GAG CCC ATC TAT CTG GGA GGG GTC TTC CAG CTG GAG			384
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu			
275	280	285	
AAG GGT GAC CGA CAG TAC ATT AAG GCC AAT TCG AAG TTC ATT GGC ATC			432
Lys Gly Asp Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile			
290	295	300	
ACT GAG CTG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC TAG			477
Thr Glu Leu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *			
305	310	315	

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
1 5 10 15	
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
20 25 30	
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
35 40 45	
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
50 55 60	
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr	
65 70 75 80	
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
85 90 95	
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
100 105 110	
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	

115		120		125
Lys Gly Asp Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile				
130		135		140
Thr Glu Leu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *				
145		150		155

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..477
- (D) OTHER INFORMATION:/codon_start= 1
/function= "Antigen"
/product= "TNF-alpha analog"
/gene= "tnfP2-7"
/standard_name= "TNF2-7"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT GAC AAG CCT GTA GCC CAT	48
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
160	165 170 175
GTT GTA GCA AAC CCT CAA GCT GAG GGG CAG CTC CAG TGG CTG AAC CGC	96
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
	180 185 190
CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG	144
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
	195 200 205
CTG GTG GTG CCA TCA GAG GGC CTG TAC CTC ATC TAC TCC CAG GTC CTC	192
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
	210 215 220
TTC AAG GGC CAA GGC TGC CCC TCC ACC CAT GTG CTC CAG TAC ATC AAA	240
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Gln Tyr Ile Lys	
	225 230 235
GCT AAC TCC AAA TTC ATC GGC ATC ACC GAA CTG GTT AAC CTC CTC TCT	288
Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Val Asn Leu Leu Ser	
240	245 250 255

GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC	336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
260 265 270	
AAG CCC TGG TAT GAG CCC ATC TAT CTG GGA GGG GTC TTC CAG CTG GAG	384
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	
275 280 285	
AAG GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG CCC GAC TAT CTC GAC	432
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	
290 295 300	
TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC TAG	477
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *	
305 310 315	

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
1 5 10 15	
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
20 25 30	
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
35 40 45	
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
50 55 60	
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Gln Tyr Ile Lys	
65 70 75 80	
Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Val Asn Leu Leu Ser	
85 90 95	
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
100 105 110	
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	
115 120 125	
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	
130 135 140	
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *	
145 150 155	

(2) INFORMATION FOR SEQ ID NO: 11:

ATG Met 160	GTC Val	AGA Arg	TCA Ser	TCT Ser	TCT Ser 165	CGA Arg	ACC Thr	CCG Pro	AGT Ser	TTC Phe 170	AAC Asn	AAT Asn	TTT Phe	ACC Thr	GTA Val 175	48
AGC Ser	TTT Phe	TGG Trp	CTC Leu	CGT Arg 180	GTA Val	CCT Pro	AAG Lys	GTG Val	TCG Ser 185	GCC Ala	TCG Ser	CAC His	CTG Leu	GAG Glu 190	CGC Arg	96
CGG Arg	GCC Ala	AAT Asn	GCC Ala 195	CTC Leu	CTG Leu	GCC Ala	AAT Asn	GGC Gly 200	GTG Val	GAG Glu	CTG Leu	AGA Arg	GAT Asp 205	AAC Asn	CAG Gln	144
CTG Leu	GTG Val	GTG Val 210	CCA Pro	TCA Ser	GAG Glu	GGC Gly	CTG Leu 215	TAC Tyr	CTC Leu	ATC Ile	TAC Tyr	TCC Ser 220	CAG Gln	GTC Val	CTC Leu	192
TTC Phe	AAG Lys 225	GGC Gly	CAA Gln	GGC Gly	TGC Cys	CCC Pro 230	TCC Ser	ACC Thr	CAT His	GTG Val	CTC Leu 235	CTC Leu	ACC Thr	CAC His	ACC Thr	240
ATC Ile 240	AGC Ser	CGC Arg	ATC Ile	GCC Ala	GTC Val 245	TCC Ser	TAC Tyr	CAG Gln	ACC Thr	AAG Lys 250	GTC Val	AAC Asn	CTC Leu	CTC Leu	TCT Ser 255	288
GCC Ala	ATC Ile	AAG Lys	AGC Ser	CCC Pro 260	TGC Cys	CAG Gln	AGG Arg	GAG Glu	ACC Thr 265	CCA Pro	GAG Glu	GGG Gly	GCT Ala	GAG Glu 270	GCC Ala	336
AAG Lys	CCC Pro	TGG Trp	TAT Tyr 275	GAG Glu	CCC Pro	ATC Ile	TAT Tyr	CTG Leu 280	GGA Gly	GGG Gly	GTC Val	TTC Phe	CAG Gln 285	CTG Leu	GAG Glu	384
AAG Lys	GGT Gly	GAC Asp	CGA Arg	CTC Leu	AGC Ser	GCT Ala	GAG Glu	ATC Ile	AAT Asn	CGG Arg	CCC Pro	GAC Asp	TAT Tyr	CTC Leu	GAC Asp	432

290	295	300	
TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC TAG			477
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *			
305	310	315	

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met	Val	Arg	Ser	Ser	Ser	Arg	Thr	Pro	Ser	Phe	Asn	Asn	Phe	Thr	Val
1				5					10					15	
Ser	Phe	Trp	Leu	Arg	Val	Pro	Lys	Val	Ser	Ala	Ser	His	Leu	Glu	Arg
			20					25					30		
Arg	Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln
		35					40					45			
Leu	Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu
	50					55					60				
Phe	Lys	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr
65					70					75					80
Ile	Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu	Leu	Ser
				85					90					95	
Ala	Ile	Lys	Ser	Pro	Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala
			100					105					110		
Lys	Pro	Trp	Tyr	Glu	Pro	Ile	Tyr	Leu	Gly	Gly	Val	Phe	Gln	Leu	Glu
		115					120					125			
Lys	Gly	Asp	Arg	Leu	Ser	Ala	Glu	Ile	Asn	Arg	Pro	Asp	Tyr	Leu	Asp
	130					135					140				
Phe	Ala	Glu	Ser	Gly	Gln	Val	Tyr	Phe	Gly	Ile	Ile	Ala	Leu	*	
145					150					155					

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..477

(D) OTHER INFORMATION:/codon_start= 1
/function= "Antigen"
/product= "TNF-alpha analog"
/gene= "tnfP30-2"
/standard_name= "TNF30-2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT GAC AAG CCT GTA GCC CAT	48
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
160 165 170 175	
GTT GTA GCA AAC CCT CAA GCT GAG GGG CAG CTC CAG TGG CTG AAC CGC	96
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
180 185 190	
CGG GCC AAT GCC CTC CTG GCC AAT TTC AAC AAC TTC ACA GTT AGC TTC	144
Arg Ala Asn Ala Leu Leu Ala Asn Phe Asn Asn Phe Thr Val Ser Phe	
195 200 205	
TGG TTG AGG GTA CCA AAG GTC TCG GCC AGC CAC CTC GAG CAG GTC CTC	192
Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Gln Val Leu	
210 215 220	
TTC AAG GGC CAA GGC TGC CCC TCC ACC CAT GTG CTC CTC ACC CAC ACC	240
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr	
225 230 235	
ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT	288
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
240 245 250 255	
GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC	336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
260 265 270	
AAG CCC TGG TAT GAG CCC ATC TAT CTG GGA GGG GTC TTC CAG CTG GAG	384
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	
275 280 285	
AAG GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG CCC GAC TAT CTC GAC	432
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	
290 295 300	
TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC TAG	477
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *	
305 310 315	

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
 1             5             10             15
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
          20             25             30
Arg Ala Asn Ala Leu Leu Ala Asn Phe Asn Asn Phe Thr Val Ser Phe
          35             40             45
Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Gln Val Leu
 50             55             60
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
 65             70             75             80
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
          85             90             95
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
          100            105            110
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
          115            120            125
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
          130            135            140
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *
145            150            155
```

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 477 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..477
(D) OTHER INFORMATION:/codon_start= 1

```

/function= "Antigen"
/product= "TNF-alpha analog"
/gene= "tnfP30-3"
/standard_name= "TNF30-3"

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT GAC AAG CCT GTA GCC CAT	48
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
160 165 170 175	
GTT GTA GCA AAC CCT CAA GCT GAG GGG CAG CTC CAG TGG CTG AAC CGC	96
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
180 185 190	
CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG	144
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
195 200 205	
CTG GTG GTG CCA TCA GAG GGC CTG TAC CTC ATC TAC TCC CAG GTC CTC	192
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
210 215 220	
TTC AAC AAC TTT ACC GTC TCC TTC TGG CTT CGG GTA CCC AAG GTC AGC	240
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser	
225 230 235	
GCT AGC CAC CTC GAG GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT	288
Ala Ser His Leu Glu Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
240 245 250 255	
GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC	336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
260 265 270	
AAG CCC TGG TAT GAG CCC ATC TAT CTG GGA GGG GTC TTC CAG CTG GAG	384
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	
275 280 285	
AAG GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG CCC GAC TAT CTC GAC	432
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	
290 295 300	
TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC TAG	477
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *	
305 310 315	

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 159 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His

1	5	10	15
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	20	25	30
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	35	40	45
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	50	55	60
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser	65	70	75
Ala Ser His Leu Glu Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	85	90	95
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	100	105	110
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	115	120	125
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	130	135	140
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *	145	150	155

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..477
 - (D) OTHER INFORMATION: /function= "Antigen"
 - /product= "TNF-alpha analog"
 - /gene= "tnfp30-4"
 - /standard_name= "TNF30-4"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT GAC AAG CCT GTA GCC CAT	160	165	170	175
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His				

GTT GTA GCA AAC CCT CAA GCT GAG GGG CAG CTC CAG TGG CTG AAC CGC	96
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
180 185 190	
CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG	144
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
195 200 205	
CTG GTG GTG CCA TCA GAG GGC CTG TAC CTC ATC TAC TCC CAG GTC CTC	192
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
210 215 220	
TTC AAG GGC CAA GGC TGC CCC TCC ACC CAT GTG CTC CTC ACC CAC ACC	240
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr	
225 230 235	
ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT	288
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
240 245 250 255	
GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA TTT AAT AAT TTC ACC	336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Phe Asn Asn Phe Thr	
260 265 270	
GTG TCC TTC TGG TTG CGC GTC CCT AAG GTA AGC GCT TCC CAC CTG GAG	384
Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu Glu	
275 280 285	
AAG GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG CCC GAC TAT CTC GAC	432
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	
290 295 300	
TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC TAG	477
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu *	
305 310 315	

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
1 5 10 15	
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
20 25 30	
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
35 40 45	
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
50 55 60	

Phe	Lys	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr	
65					70					75					80	
Ile	Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu	Leu	Ser	
				85					90					95		
Ala	Ile	Lys	Ser	Pro	Cys	Gln	Arg	Glu	Thr	Pro	Phe	Asn	Asn	Phe	Thr	
			100					105					110			
Val	Ser	Phe	Trp	Leu	Arg	Val	Pro	Lys	Val	Ser	Ala	Ser	His	Leu	Glu	
		115					120					125				
Lys	Gly	Asp	Arg	Leu	Ser	Ala	Glu	Ile	Asn	Arg	Pro	Asp	Tyr	Leu	Asp	
	130					135					140					
Phe	Ala	Glu	Ser	Gly	Gln	Val	Tyr	Phe	Gly	Ile	Ile	Ala	Leu	*		
145					150					155						

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..477
- (D) OTHER INFORMATION:/codon_start= 1
/function= "Antigen"
/product= "TNF-alpha analog"
/gene= "tnfp30-5"
/standard_name= "TNF30-5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATG	GTC	AGA	TCA	TCT	TCT	CGA	ACC	CCG	AGT	GAC	AAG	CCT	GTA	GCC	CAT	48
Met	Val	Arg	Ser	Ser	Ser	Arg	Thr	Pro	Ser	Asp	Lys	Pro	Val	Ala	His	
160					165					170					175	
GTT	GTA	GCA	AAC	CCT	CAA	GCT	GAG	GGG	CAG	CTC	CAG	TGG	CTG	AAC	CGC	96
Val	Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg	
			180					185					190			
CGG	GCC	AAT	GCC	CTC	CTG	GCC	AAT	GGC	GTG	GAG	CTG	AGA	GAT	AAC	CAG	144
Arg	Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	
			195					200				205				
CTG	GTG	GTG	CCA	TCA	GAG	GGC	CTG	TAC	CTC	ATC	TAC	TCC	CAG	GTC	CTC	192
Leu	Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	

210	215	220	
TTC AAG GGC CAA GGC TGC CCC TCC ACC CAT GTG CTC CTC ACC CAC ACC			240
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr			
225	230	235	
ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT			288
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser			
240	245	250	255
GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC			336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala			
	260	265	270
AAG CCC TGG TAT GAG CCC ATC TAT CTG GGA GGG GTC TTC CAG CTG GAG			384
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu			
	275	280	285
AAG GGT GAC CGA TTC AAC AAT TTC ACC GTA AGC TTC TGG CTT CGC GTC			432
Lys Gly Asp Arg Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val			
	290	295	300
CCT AAG GTG TCT GCG TCG CAC CTC GAA GGG ATC ATT GCC CTC TAG			477
Pro Lys Val Ser Ala Ser His Leu Glu Gly Ile Ile Ala Leu *			
305	310	315	

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Met	Val	Arg	Ser	Ser	Ser	Arg	Thr	Pro	Ser	Asp	Lys	Pro	Val	Ala	His
1				5					10					15	
Val	Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg
			20					25					30		
Arg	Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln
		35					40					45			
Leu	Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu
	50					55					60				
Phe	Lys	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr
65					70					75					80
Ile	Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu	Leu	Ser
			85					90						95	
Ala	Ile	Lys	Ser	Pro	Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala
		100						105					110		
Lys	Pro	Trp	Tyr	Glu	Pro	Ile	Tyr	Leu	Gly	Gly	Val	Phe	Gln	Leu	Glu

115	120	125
Lys Gly Asp Arg Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val		
130	135	140
Pro Lys Val Ser Ala Ser His Leu Glu Gly Ile Ile Ala Leu *		
145	150	155

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:1..24
 - (C) IDENTIFICATION METHOD: experimental
 - (D) OTHER INFORMATION:/function= "Primer for PCR cloning of DNA encoding TNF-alpha"
 /product= "Primer binding to TNF-alpha gene"
 /evidence= EXPERIMENTAL
 /standard_name= "TNF-alpha Primer I"
 /label= Primer1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GACAAGCCCA TGGTCAGATC ATCT

24

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:1..30
 - (C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION:/function= "Primer for PCR cloning
of DNA encoding TNF-alpha"
/product= "Primer binding to TNF-alpha gene"
/evidence= EXPERIMENTAL
/standard_name= "TNF-alpha Primer II"
/label= Primer2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TCTCTAGAGG GCAATGATCC CAAAGTAGAC

30

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION:1..21
(C) IDENTIFICATION METHOD: experimental
(D) OTHER INFORMATION:/function= "Primer for PCR cloning
of DNA encoding TNF-alpha"
/product= "Primer binding to TNF-alpha gene"
/evidence= EXPERIMENTAL
/standard_name= "TNF-alpha Primer III"
/label= Primer3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CCCAAAGTAG ACCTGCCCAG A

21

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: insertion_seq
- (B) LOCATION:7..51
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/function= "Primer for PCR cloning
of DNA encoding TNF-alpha analog"
/evidence= EXPERIMENTAL
/organism= "Homo sapiens"
/standard_name= "Primer "mut2-1""
/label= mut2-1
/note= "Primer "mut2-1" is a synthetically synthesised
69-mer oligonucleotide comprising DNA encoding the human
T cell epitope P2 between stretches of DNA homologous to
stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

ACCCCGAGTC AGTACATTAA AGCCAATTCT AAATTCATCG GTATAACTGA GCTGCAGCTC	60
CAGTGGCTG	69

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: insertion_seq
 - (B) LOCATION:15..59
 - (C) IDENTIFICATION METHOD: experimental
 - (D) OTHER INFORMATION:/function= "Primer for PCR cloning
of DNA encoding TNF-alpha analog"
/evidence= EXPERIMENTAL
/organism= "Homo sapiens"
/standard_name= "Primer "mut2-3""
/label= mut2-3
/note= "Primer "mut2-3" is a synthetically synthesised
73-mer oligonucleotide comprising DNA encoding the human
T cell epitope P2 between stretches of DNA homologous to
stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CCCAGGTCCT CTTCCAGTAC ATAAAGGCCA ACTCCAAGTT TATCGGCATC ACCGAGCTCA	60
TCAGCCGCAT CGC	73

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: insertion_seq
 - (B) LOCATION:12..56
 - (C) IDENTIFICATION METHOD: experimental
 - (D) OTHER INFORMATION:/function= "Primer for PCR cloning of DNA encoding TNF-alpha analog"
 /evidence= EXPERIMENTAL
 /organism= "Homo sapiens"
 /standard_name= "Primer "mut2-4"
 /label= mut2-4
 /note= "Primer "mut2-4" is a synthetically synthesised 75-mer oligonucleotide comprising DNA encoding the human T cell epitope P2 between stretches of DNA homologous to stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

AGTCGGTCAC CGAGCTCCGT GATGCCGATG AATTTCAAT TGGCCTTGAT ATACTGGGGC	60
TTGGCCTCAG CCCCC	75

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: insertion_seq
 - (B) LOCATION:8..52
 - (C) IDENTIFICATION METHOD: experimental
 - (D) OTHER INFORMATION:/function= "Primer for PCR cloning of DNA encoding TNF-alpha analog"
 /evidence= EXPERIMENTAL

/organism= "Homo sapiens"
/standard_name= "Primer "mut2-5"
/label= mut2-5
/note= "Primer "mut2-5" is a synthetically synthesised
75-mer oligonucleotide comprising DNA encoding the human
T cell epitope P2 between stretches of DNA homologous to
stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GAAGGGTGAC CGACAGTACA TTAAGGCCAA TTCGAAGTTC ATTGGCATCA CTGAGCTGTC 60
TGGGCAGGTC TACTT 75

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: insertion_seq
- (B) LOCATION:14..58
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/function= "Primer for PCR cloning
of DNA encoding TNF-alpha analog"
/evidence= EXPERIMENTAL
/organism= "Homo sapiens"
/standard_name= "Primer "mut2-7"
/label= mut2-7
/note= "Primer "mut2-7" is a synthetically synthesised
80-mer oligonucleotide comprising DNA encoding the human
T cell epitope P2 between stretches of DNA homologous to
stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CACCCATGTG CTCCAGTACA TCAAAGCTAA CTCCAAATTC ATCGGCATCA CCGAACTGGT 60
TAACCTCCTC TCTGCCATCA 80

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: insertion_seq
 - (B) LOCATION:10..72
 - (C) IDENTIFICATION METHOD: experimental
 - (D) OTHER INFORMATION:/function= "Primer for PCR cloning
of DNA encoding TNF-alpha analog"
/evidence= EXPERIMENTAL
/organism= "Homo sapiens"
/standard_name= "Primer "mut30-1"
/label= mut30-1
/note= "Primer "mut30-1" is a synthetically synthesised
96-mer oligonucleotide comprising DNA encoding the human
T cell epitope P30 between stretches of DNA homologous to
stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```
ACCCCGAGTT TCAACAATTT TACCGTAAGC TTTTGGCTCC GTGTACCTAA GGTGTCGGCC      60
TCGCACCTGG AGCGCCGGGC CAATGCCCTC CTGGCC                                96
```

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: insertion_seq
 - (B) LOCATION:12..74
 - (C) IDENTIFICATION METHOD: experimental
 - (D) OTHER INFORMATION:/function= "Primer for PCR cloning
of DNA encoding TNF-alpha analog"
/evidence= EXPERIMENTAL
/organism= "Homo sapiens"
/standard_name= "Primer "mut30-2"
/label= mut30-2

/note= "Primer "mut30-2" is a synthetically synthesised 100-mer oligonucleotide comprising DNA encoding human T cell epitope P30 between stretches of DNA homologous to stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

TCCTGGCCAA TTTCAACAAC TTCACAGTTA GCTTCTGGTT GAGGGTACCA AAGGTCTCGG 60
CCAGCCACCT CGAGCAGGTC CTCTTCAAGG GCCAAGGCTG 100

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: insertion_seq
- (B) LOCATION:12..74
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/function= "Primer for PCR cloning of DNA encoding TNF-alpha analog"
/evidence= EXPERIMENTAL
/organism= "Homo sapiens"
/standard_name= "Primer "mut30-3""
/label= mut30-3
/note= "Primer "mut30-3" is a synthetically synthesised 100-mer oligonucleotide comprising DNA encoding human T cell epitope P30 between stretches of DNA homologous to stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CCCAGGTCCT CTTCAACAAC TTTACCGTCT CCTTCTGGCT TCGGGTACCC AAGGTCAGCG 60
CTAGCCACCT CGAGGTCTCC TACCAGACCA AGGTCAACCT 100

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: insertion_seq

(B) LOCATION:15..77

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION:/function= "Primer for PCR cloning
of DNA encoding TNF-alpha analog"
/evidence= EXPERIMENTAL
/organism= "Homo sapiens"
/standard_name= "Primer "mut30-4"
/label= mut30-4
/note= "Primer "mut30-4" is a synthetically synthesised
100-mer oligonucleotide comprising DNA encoding human T
cell epitope P30 between stretches of DNA homologous to
stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```
AGTCGGTCAC CCTTCTCCAG GTGGGAAGCG CTTACCTTAG GGACGCGCAA CCAGAAGGAC      60
ACGGTGAAAT TATTAAATGG GGTCTCCCTC TGGCAGGGGC                          100
```

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: insertion_seq

(B) LOCATION:14..76

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION:/function= "Primer for PCR cloning
of DNA encoding TNF-alpha analog"
/evidence= EXPERIMENTAL
/organism= "Homo sapiens"
/standard_name= "Primer "mut30-5"
/label= mut30-5
/note= "Primer "mut30-5" is a synthetically synthesised
100-mer oligonucleotide comprising DNA encoding human T
cell epitope P30 between stretches of DNA homologous to
stretches of the human TNF-alpha gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GAAGGGTGAC CGATTCAACA ATTTACCGT AAGCTTCTGG CTTGCGTCC CTAAGGTGTC 60
TGGTTCGCAC CTCGAAGGGA TCATTGCCCT CTAGAGTCGA 100

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION:1..25
- (D) OTHER INFORMATION:/label= Pep2-1
/note= "Pep2-1 is a synthetically prepared truncated form
of a TNF-alpha analog comprising the human T cell epitope
P2 and flanking portions of human TNF-alpha"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Ser Arg Thr Pro Ser Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly
1 5 10 15
Ile Thr Glu Leu Gln Leu Gln Trp Leu
 20 25

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION:1..25
- (D) OTHER INFORMATION:/label= Pep2-3
/note= "Pep2-3 is a synthetically prepared truncated form
of a TNF-alpha analog comprising the human T cell epitope
P2 and flanking portions of human TNF-alpha"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Ser Gln Val Leu Phe Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly
1 5 10 15
Ile Thr Glu Leu Ile Ser Arg Ile Ala
 20 25

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION:1..25
 - (D) OTHER INFORMATION:/label= Pep2-4
/note= "Pep2-4 is a synthetically prepared truncated form
of a TNF-alpha analog comprising the human T cell epitope
P2 and flanking portions of human TNF-alpha"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Ala Glu Ala Lys Pro Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly
1 5 10 15
Ile Thr Glu Leu Gly Asp Arg Leu Ser
 20 25

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION:1..25

(D) OTHER INFORMATION:/label= Pep2-5

/note= "Pep2-5 is a synthetically prepared truncated form
of a TNF-alpha analog comprising the human T cell epitope
P2 and flanking portions of human TNF-alpha"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Glu	Lys	Gly	Asp	Arg	Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly
1				5					10					15	
Ile	Thr	Glu	Leu	Ser	Gly	Gln	Val	Tyr							
			20					25							

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION:1..31

(D) OTHER INFORMATION:/label= Pep30-1

/note= "Pep30-1 is a synthetically prepared truncated
form of a TNF-alpha analog comprising human T cell
epitope P30 and flanking portions of human TNF-alpha"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Ser	Arg	Thr	Pro	Ser	Phe	Asn	Asn	Phe	Thr	Val	Ser	Phe	Trp	Leu	Arg
1				5					10					15	
Val	Pro	Lys	Val	Ser	Ala	Ser	His	Leu	Glu	Arg	Arg	Ala	Asn	Ala	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION:1..31

(D) OTHER INFORMATION:/label= Pep30-2

/note= "Pep30-2 is a synthetically prepared truncated
form of a TNF-alpha analog comprising the human T cell
epitope P30 and flanking portions of human TNF-alpha"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Ala Leu Leu Ala Asn Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg
1 5 10 15

Val Pro Lys Val Ser Ala Ser His Leu Glu Gln Val Leu Phe Lys
20 25 30

B¹
(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION:1..31

(D) OTHER INFORMATION:/label= Pep30-3

/note= "Pep30-3 is a synthetically prepared truncated
form of a TNF-alpha analog comprising the human T cell
epitope P30 and flanking portions of human TNF-alpha"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Tyr Ser Gln Val Leu Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg
1 5 10 15

Val Pro Lys Val Ser Ala Ser His Leu Glu Val Ser Tyr Gln Thr
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION:1..31
 - (D) OTHER INFORMATION:/label= Pep30-4
 /note= "Pep30-4 is a synthetically prepared truncated form of a TNF-alpha analog comprising the human T cell epitope P30 and flanking portions of human TNF-alpha"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Gln Arg Glu Thr Pro Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg
 1 5 10 15
 Val Pro Lys Val Ser Ala Ser His Leu Glu Lys Gly Asp Arg Leu
 20 25 30

B! (2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION:1..31
 - (D) OTHER INFORMATION:/label= Pep30-5
 /note= "Pep30-5 is a synthetically prepared truncated

form of a TNF-alpha analog comprising the human T cell
epitope P30 and flanking portions of human TNF-alpha"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

B¹

Glu	Lys	Gly	Asp	Arg	Phe	Asn	Asn	Phe	Thr	Val	Ser	Phe	Trp	Leu	Arg
1				5					10					15	
Val	Pro	Lys	Val	Ser	Ala	Ser	His	Leu	Glu	Gly	Ile	Ile	Ala	Leu	
			20					25					30		
